

SEQ. ID 3-1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTGAAGGATCT 60
 SEQ. ID 4-1 M T F N S F E G S 9

61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA 120
 10 K T C V P A D I N K E E E F V E E F N R 29

121 TTAAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACGA 180
 30 L K T F A N F P S G S P V S A S T L A R 49

181 GCAGGGTTTCTTTATACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTCATGCAGCT 240
 50 A G F L Y T G E G D T V R C F S C H A A 69

241 GTAGATAGATGGCAATATGGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT 300
 70 V D R W Q Y G D S A V G R H R K V S P N 89

301 TGCAGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCACGCAGTCTACAAATTCTGGT 360
 90 C R F I N G F Y L E N S A T Q S T N S G 109

361 ATCCAGAATGGTCAGTACAAAGTTGAAAATCTCTGGGAAGCAGAGATCATTTCGCCTTA 420
 110 I Q N G Q Y K V E N Y L G S R D H F A L 129

421 GACAGGCCATCTGAGACACATGCAGACTATCTTTGAGAACTGGGCAGGTTGTAGATATA 480
 130 D R P S E T H A D Y L L R T G Q V V D I 149

481 TCAGACACCATATACCCGAGGAACCCTGCCATGTATaGTGAAGAAGCTAGATTAAAGTCC 540
 150 S D T I Y P R N P A M Y S E E A R L K S 169

541 TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTGCTGGACTC 600
 170 F Q N W P D Y A H L T P R E L A S A G L 189

601 TACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGTGTGGTGGAAAATGAAAAT 660
 190 Y Y T G I G D Q V Q C F C C G G K L K N 209

661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTGCTTCTTT 720
 210 W E P C D R A W S E H R R H F P N C F F 229

721 GTTTTGGGCCGAATCTTAATATTGCAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780
 230 V L G R N L N I R S E S D A V S S D R N 249

781 TTCCCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC 840
 250 F P N S T N L P R N P S M A D Y E A R I 269

841 TTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTT 900
 270 F T F G T W I Y S V N K E Q L A R A G F 289

901 TATGCTTTAG^{1,2}GTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGCTAACTGAT 960
 290 Y A L G E G D K V K C F H C G G G L T D 309

961 TGGAAGCCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGG^{2,3}GTGCAAATAT 1020
 310 W K P S E D P W E Q H A K W Y P G C K Y 329

1021 CTGTTAGAACAGAAGGGACAAGAATATATAAACAATATTCATTAACTCATTCACTTGAG 1080
 330 L L E Q K G Q E Y I N N I H L T H S L E 349

Fig. 1

T0609T "26542660

Fig. 1 (cont.)

3061 AATATTGGCAAGAAAAGAAGAATAGTTGTTTAAATATTTTTTAAAAAACACTTGAATAAG 3120
 3121 AATCAGTAGGGTATAAACTAGAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACAT 3180
 3181 TACAAGATTCTCACAACAAACCCATTGTAGAGGTGAGTAAGGCATGTTACTACAGAGGAA 3240
 3241 AGTTTGAGAGTAAACTGTAAAAATTATATTTTTGTTGTACTTTCTAAGAGAAAAGAGTA 3300
 3301 TTGTTATGTTCTCCTAACTTCTGTTGATTACTACTTTAAGTGATATTCATTTAAACATT 3360
 3361 GCAAATTTATTTTATTTTATTTTAAATTTTCTTTTGAGATGGAGTCTTGCTTGTCAACCAGG 3420
 3421 CTGGAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCTTCTGGGTTCAAGCGAT 3480
 3481 TCTCGTGCCTCAGCTTCTGAGTAGCTGGAATTACAGGCAGGTGCCACCATGCCCGACTA 3540
 3541 ATTTTATTTTATTTTATTTTATTTTAAATTTTCTTTTGAGATGGAGTCTTGCTTGTCAACCAGG 3600
 3601 TCCTGACCTCAAGAGATCCACTCGCCTTGCCCTCCCAAAGTGCTGGGATTACAGGCTTGA 3660
 3661 GCCACCACGCCCGCTAAAAACATTGCAAATTTAAATGAGAGTTTTAAAAATTAAATAATG 3720
 3721 ACTGCCCTGTTTCTGTTTTAGTATGTAAATCCTCAGTTCCTCACCTTTGCACTGTCTGCC 3780
 3781 ACTTAGTTGGTTATATAGTCATTAACCTGAATTTGGTCTGTATAGTCTAGACTTTAAAT 3840
 3841 TTAAAGTTTCTACAAGGGGAGAAAAGTGTTAAATTTTAAATATGTTTCCAGGACA 3900
 3901 CTTCACTTCCAAGTCAGGTAGGTAGTTCATCTAGTTGTTAGCCAAGGACTCAAGGACTG 3960
 3961 AATTGTTTAAACATAAGGCTTTTCTGTTCTGGGAGCCGCACTTCATTAATAATTCTTCTA 4020
 4021 AAACCTGTATGTTTAGAGTTAAGCAAGACTTTTTTCTTCTCCTCTCCATGAGTTGTGAAAT 4080
 4081 TTAATGCACAACGCTGATGTGGCTAACAAGTTTATTTTAAAGATTGTTTAGAAATGCTGT 4140
 4141 TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACCTTAATCAAATTTTGGAGACTTA 4200
 4201 ACAGCATTGTCTGTGTTTGAACATAAAAAGCACCGGATCTTTCCATCTAATTCCGCA 4260
 4261 AAAATTGATCATTTGCAAAGTCAAAACTATAGCCATATCCAAATCTTTCCCCCTCCCAA 4320
 4321 GAGTTCTCAGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTCACTCTAGGATTT 4380
 4381 CAAGTCACCACTTATTTTACATTTTAGTCATGCAAAGATTCAAGTAGTTTGCATAAAGT 4440
 4441 ACTTATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAGCATTGTCTTAATTTTGGAG 4500
 4501 AACTGGTTTTAGCATTTACAACTAAATTCAGTTAATTAATTAATAGCTTTATATTGCC 4560
 4561 TTTCTGTCTACATTTGGTTTTTCCCTGTCCCTTTGATTACGGGCTAAGGTAGGGTAAG 4620
 4621 AXXGGGTGTAGTGAGTGTATATAATGTGATTTGGCCCTGTGTATTATGATTTTTGTTAT 4680
 4681 TTTTGTGTTATATTATTTACATTTTCAAGTGTGTTTTTGTGTTTCCATTTTAGGGGAT 4740
 4741 AAAATTTGTATTTTGAACATATGAATGGAGACTACCGCCCCAGCATTAGTTTCACATGATA 4800
 4801 TACCCTTTAAACCCGAATCATTGTTTTATTTCTGATTACACAGGTGTTGAATGGGGAAA 4860
 4861 GGGGCTAGTATATCAGTAGGATATACTATGGGATGTATATATATCATTGCTGTTAGAGAA 4920
 4921 ATGAAATAAATGGGGCTGGGCTCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGG 4980
 4981 CTGAGGCAGGTGGATCACGAGGTGAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC 5040
 5041 CCCGTCTCTACTAAAAACAGAAAATTAGCCGGCGTGGTGGCGGGCGCCTGTAGTCCCA 5100
 5101 GCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCAGAGCTTGCACTGA 5160
 5161 GCCGAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAA 5220
 5221 AAAAAAAAAAAG 5232

Fig. 1 (cont.)

SEQ. ID 5-1 TTGCTCTGTCACCCAGTTTGGAGTGCAGTTATGCAGTCTCACACTGCAAGCTCTGCCTCA 60
61 TGGGCTCAAGTGAACCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACCACAGGCAGGTGCC 120
121 ACCATGTCTGGCTAATTTTTGAGTTTCTTTGTAGAGATGGTGTGTTTGCCAAGTCACCCAG 180
181 TTTGAGGCTGGTCTCAAACACCTGGGCTCAAGCAATCCATCTACCTCAGCCTCCCAAGT 240
241 GCTGGGATTACAGGAGTGAGCCATGGCATGAGGCCTTGTGGGGTGTCTCTTTTAAATGAA 300
301 AGCATACTCTGTTTACGTATTTGATATGAAGGAATATCCTTCCTTTCCACAAAGACAAAA 360
361 ATTATCCTATTTTTCTCAAAACATATGTCCTTTTTCTCTACTTTTCATTTTGTACTTT 420
421 TGATGGACACATGTGTTACATTGATTTCACTTTCTCATAATTCTGCTGTAAGAAAAACAA 480
481 TAGTGCCAGTTCATGACAAATAGCAACAGTCTGTTATTGCTAGACTGTTACTGTTAGTG 540
541 GAGACTACCAGAACAGTCAGTCCCAGTGTCAGGGAATCAAAGAGAACATGTTCCCTCTCT 600
601 AAAGGGCAGAGCTGCTGCTCAGCTTTAGCTGATTGCTGCCCTGCAGGACTATAGGCCCCAG 660
661 TGTTGCTAGATCTTTTGATGTTTCAAGAGAAGCTTGGAACTAGAAATGTGATGGGAAGTC 720
721 TCTTACATTTAAACATGTTGGCAATTAATGGTAAGATTTAAAAATACTGTGGTCCAAGAA 780
781 AAAAATGGATTTGGAACTGGATTAAATCAAATGAGGCATGCAGATTAATCTACAGCAT 840
841 GGTACAATGTGAATTTCTGGTTCTTTAATTGCACTGTAATTAGGTAAGATGTTAGCTT 900
901 TGGGGAAGCTAAGTGCAGAGTATGCAGAACTATTATTTTTGTAAGTTTTCTCTAAGTAT 960
961 AAATAAATTTCAAATAAAAAATAAACTTAGTAAAGAACTATAATGCAATTCATGTAA 1020
1021 GCCAAACATAATATGTCTTCCAGTTTGAAACCTCTGGGTTTTATTTTATTTTATTTTATT 1080
1081 TTTGAGACAGAGTCTTGCTGTGTCAACCAGGCTGGAGTGTAGTGGCACTATTTTCGGCCCA 1140
1141 CTGCAACCTCCACCTCCCAGGCTCAAATGATTCTCCTGCCTCAGCCTCCGGAGTAGCTGG 1200
1201 GATTACAGGCGCGTACCACCACCCAGCTAATTTTTGTATTTTAGTAGAGATGGGGTT 1260
1261 TCACCATTTTGGCCAGGCTGGTTTTGAACTCCTGACCTCAAGTGATCCACTTGTCTTGGC 1320
1321 CTCCCAAATGCTGGGATTACAGGCGTGAGCCACTGCACCAGGCAGAGGCCTCTGTTTTT 1380
1381 TATCTCTTTTGGCCTCTACAGTGCCTAGTAAAGCACCTGATACATGGTAAACGATCAGT 1440
1441 AATTACTAGTACTTATTTTGGAGAAATGATTTTTTAAAAAGTCATTGTGTTCCATCCA 1500
1501 TGAGTCGTTTGAAGTTTTAAACTGTCTTTTTGTTTGTGTTTTGAACAGGTTTACAAAGGAG 1560
1561 GAAAACGACTTCTTCTAGATTTTTTTTTTTCAGTTTCTTCTATAAATCAAACATCTCAAAA 1620
1621 TGGAGACCTAAAATCCTTAAAGGGACTTAGTCTAATCTCGGGAGGTAGTTTTGTGCATGG 1680
1681 GTAAACAAATTAAGTATTAAGTGGTGTGTTTACTATCCAAAGAATGCTAATTTTATAAACA 1740
1741 TGATCGAGTTATATAAGGTATACCATAATGAGTTTGATTTTGAATTTGATTTGTGGAAAT 1800
1801 AAAGGAAAAGTGATTCTAGCTGGGGCATATTGTTAAAGCATTTTTTTTCAGAGTTGGCCAG 1860
1861 GCAGTCTCCTACTGGCACATTCTCCCATTAATGTAGAATAGAAATAGTACCTGTGTTTGGG 1920
1921 AAAGATTTTAAAATGAGTGACAGTTATTTGGAACAAAAGAGCTAATAATCAATCCACTGCA 1980
1981 AATTAAAGAAACATGCAGATGAAAGTTTTGACACATTAATACTTCTACAGTGACAAAG 2040
2041 AAAAATCAAGAACAAAGCTTTTTGATATGTGCAACAAATTTAGAGGAAGTAAAAAGATAA 2100
2101 ATGTGATGATTGGTCAAGAAATTATCCAGTTATTTACAAGGCCACTGATATTTTAAACGT 2160
2161 CCAAAAGTTTGTGTTAAATGGGCTGTTACCGCTGAGAATGATGAGGATGAGAATGATGGTT 2220
2221 GAAGGTTACATTTTAGGAAATGAAGAACTTAGAAAATTAATATAAAGACAGTGATGAAT 2280
2281 ACAAAGAAGATTTTATAACAATGTGTAAATTTTTGGCCAGGGAAAGGAATATTGAAGT 2340
2341 TAGATACAATTACTTACCTTTGAGGGAATAATTGTTGGTAATGAGATGTGATGTTTCTC 2400
2401 CTGCCACCTGGAAAACAAAGCATTGAAGTCTGCAGTTGAAAAGCCCAACGTCTGTGAGATC 2460
2461 CAGGAAACCATGCTTGCAACCACTGGTAAAAAAAAAAAAAAAAAAAAAGCCACAG 2520
2521 TGACTTGCTTATTGGTCATTGCTAGTATTATCGACTCAGAACCTCTTTACTAATGGCTAG 2580
2581 TAAATCATAATTGAGAAATTCTGAATTTTGACAAGGTCTCTGCTGTTGAAATGGTAAATT 2640
2641 TATTATTTTTTTGTCATGATAAATTCTGGTTCAAGGTATGCTATCCATGAAATAATTTT 2700
2701 TGACCAAACTAAATTGATGCAATTTGATTATCCATCTTAGCCTACAGATGGCATCTGGT 2760
2761 AACTTTTGACTGTGTTTAAAAATAAATCCACTATCAGAGTAGATTTGATGTTGGCTTCAG 2820
2821 AAACATTTAGAAAAACAAAGTTCAAAAATGTTTTCAGGAGGTGATAAGTTGAATAACTC 2880
2881 TACAATGTTAGTTCTTTGAGGGGGACAAAAATTTAAATCTTTGAAAGGTCTTATTTTA 2940
2941 CAGCCATATCTAAATTATCTTAAGAAAATTTTAAACAAAGGAATGAAATATATATCATG 3000
3001 ATTCGTGTTTTCCAAAAGTAACCTGAATATAGCAATGAAGTTCAGTTTGTATTGGTAG 3060
3061 TTTGGGCAGAGTCTCTTTTGCAGCACCTGTTGTCTACCATAATTACAGAGGACATTTCC 3120
3121 ATGTTCTAGCCAAGTATACTATTAGAATAAARAACTTAACATTGAGTTGCTTCAACAGC 3180

Fig. 2

3181 ATGAAACTGAGTCCAAAAGACCAAATGAACAAACACATTAATCTCTGATTATTTATTTTA 3240
 3241 AATAGAATATTTAATTGTGTAAGATCTAATAGTATCATTATACTTAAGCAATCATATTCC 3300
 3301 TGATGATCTATGGGAAATAACTATTATTTAATTAATATTGAAACCAGGTTTAAAGATGTG 3360
 3361 TTAGCCAGTCCTGTTACTAGTAAATCTCTTTATTTGGAGAGAAATTTTAGATTGTTTTGT 3420
 3421 TCTCCTTATTAGAAGGATTGTAGAAAGAAAAAATGACTAATTGGAGAAAAATTGGGGAT 3480
 3481 ATATCATATTTCACTGAATTCAAATGTCTTCAGTTGTAAATCTTACCATTATTTTACGT 3540
 3541 ACCTCTAAGAAATAAAAGTGCTTCTAATTAATAATATGATGTCATTAATTATGAAATACTT 3600
 3601 CTTGATAACAGAAGTTTTAAAATAGCCATCTTAGAATCAGTGAAATATGGTAATGTATTA 3660
 3661 TTTTCCTCCTTTGAGTNAGGTCTGTGCTTTTTNTTCCTGGCCACTAAATNTCACCATNT 3720
 3721 CCAANAAGCAAANTAAACCTATTCTGAATATTTTTGCTGTGAAACACTTGNCAGCAGAGC 3780
 3781 TTTCCCNCCATGNNAGAAGCTTCATGAGTCACACATTACATCTTTGGGTGATTGAATGC 3840
 3841 CACTGAAACATTTCTAGTAGCCTGGAGNAGTTGACCTACCTGTGGAGATGCCCTGCCATTA 3900
 3901 AATGGCATCCTGATGGCTTAATACACATCACTCTTCTGTGNAGGGTTTTAATTTCAACA 3960
 3961 CAGCTTACTCTGTAGCATCATGTTTACATTGTATGTATAAAGATTATACNAAGGTGCAAT 4020
 4021 TGTGTATTTCTTCCTTAAATGTATCAGTATAGGATTTAGAATCTCCATGTTGAAACTCT 4080
 4081 AAATGCATAGAAATAAAAAATAATAAAAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTA 4140
 4141 AAAGTATAAAGCAAAGCCATGCACAAAACCTACCTCCCTAGAGAAAGGCTAGTCCCTTT 4200
 4201 TCTTCCCCATTCAATTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAATTTGA 4260
 SEQ. ID 6-1 M N I V E N S I F L S N L M 14
 4261 TGAAAAGCGCCAACACGTTTGAACGTGAAATACGACTTGTCATGTGAACGTGACCGAATGT 4320
 15 K S A N T F E L K Y D L S C E L Y R M S 34
 4321 CTACGTATTCCACTTTTCCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGCTG 4380
 35 T Y S T F P A G V P V S E R S L A R A G 54
 4381 GTTCTATTACACTGGTGTGAATGACAAGGTCAAATGCTTCTGTTGTGGCCTGATGCTGG 4440
 55 F Y Y T G V N D K V K C F C C G L M L D 74
 4441 ATAACGTGAAAAGAGGAGACAGTCCTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCA 4500
 75 N W K R G D S P T E K H K K L Y P S C R 94
 4501 GATTCGTTCAAGTCTAAATTCGGTTAACAACCTGGAAGCTACCTCTCAGCCTACTTTTC 4560
 95 F V Q S L N S V N N L E A T S Q P T F P 114
 4561 CTTCTTCAGTAACACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATT 4620
 115 S S V T H S T H S L L P G T E N S G Y F 134
 4621 TCCGTGGCTCTTATTCAAACCTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAAT 4680
 135 R G S Y S N S P S N P V N S R A N Q E F 154
 4681 TTTCTGCCTTGATGAGAAGTTCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTAC 4740
 155 S A L M R S S Y P C P M N N E N A R L L 174
 4741 TTACTTTTCAGACATGGCCATTGACTTTTCTGTGCGCAACAGATCTGGCAGCAGCAGGCT 4800
 175 T F Q T W P L T F L S P T D L A R A G F 194
 4801 TTTACTACATAGGACCTGGAGACAGAGTGGCTTGCTTTGCCTGTGGTGGAAAATTGAGCA 4860
 195 Y Y I G P G D R V A C F A C G G K L S N 214
 4861 ATTGGGAACCGAAGGATAATGCTATGTGAGAACACCTGAGACATTTTCCCAAATGCCCAT 4920
 215 W E P K D N A M S E H L R H F P K C P F 234

Fig. 2 (cont.)

4921 TTATAGAAAATCAGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGA 4980
 235 I E N Q L Q D T S R Y T V S N L S M Q T 254
 4981 CACATGCAGCCCGCTTTAAACATTCTTTAACTGGCCCTCTAGTGTCTAGTTAATCCTG 5040
 255 H A A R F K T F F N W P S S V L V N P E 274
 5041 AGCAGCTTGCAAGTGC GGGTTTTTATTATGTGGTAACAGTGATGATGTCAAATGCTTTT 5100
 275 Q L A S A G F Y Y V G N S D D V K C F C 294
 5101 GCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCACATGCCA 5160
 295 C D G G L R C W E S G D D P W V Q H A K 314
 5161 AGTGGTTTCCAAGGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTCATCCGTCAAG 5220
 315 W F P R C E Y L I R I K G Q E F I R Q V 334
 5221 TTCAAGCCAGTTACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCCAGGAG 5280
 335 Q A S Y P H L L E Q L L S T S D S P G D 354
 5281 ATGAAAATGCAGAGTCATCAATTATCCATTTTGAACCTGGAGAAGACCATTGAGAAGATG 5340
 355 E N A E S S I I H F E P G E D H S E D A 374
 5341 CAATCATGATGAATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCC 5400
 375 I M M N T P V I N A A V E M G F S R S L 394
 5401 TGGTAAAACAGACAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAATTATAGACTAGTCA 5460
 395 V K Q T V Q R K I L A T G E N Y R L V N 414
 5461 ATGATCTTGTGTTAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGGAGAGAGAAA 5520
 415 D L V L D L L N A E D E I R E E E R E R 434
 5521 GAGCAACTGAGGAAAAAGAATCAATATGATTTATTATTAATCCGGAAGAATAGAATGGCAC 5580
 435 A T E E K E S N D L L L I R K N R M A L 454
 5581 TTTTCAACATTTGACTTGTGTAATCCAATCCTGGATAGTCTACTAACTGCCGGAATTA 5640
 455 F Q H L T C V I P I L D S L L T A G I I 474
 5641 TTAATGAACAAGAACATGATGTTATTAAACAGAAGACACAGACGTCTTTACAAGCAAGAG 5700
 475 N E Q E H D V I K Q K T Q T S L Q A R E 494
 5701 AACTGATTGATACGATTTTAGTAAAAGGAAATATTGCAGCCACTGTATTCAGAAACTCTC 5760
 495 L I D T I L V K G N I A A T V F R N S L 514
 5761 TGCAAGAAGCTGAAGCTGTGTTATATGAGCATTTATTTGTGCAACAGGACATAAAATATA 5820
 515 Q E A E A V L Y E H L F V Q Q D I K Y I 534
 5821 TTCCACAGAAGATGTTTCAGATCTACAGTGGAAGAACAATTGCGGAGACTACAAGAAG 5880
 535 P T E D V S D L P V E E Q L R R L Q E E 554
 5881 AAAGAACATGTAAAGTGTGTATGGACAAAGAAGTGCCATAGTGTATTTCCTTGTGGTC 5940
 555 R T C K V C M D K E V S I V F I P C G H 574
 5941 ATCTAGTAGTATGCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCCTATTGTAGGAGTA 6000
 575 L V V C K D C A P S L R K C P I C R S T 594

Fig. 2 (cont.)

6001 CAATCAAGGGTACAGTTCGTACATTTCTTTCATGAAGAAGAACC AAAACATCGTCTAAAC 6060
595 I K G T V R T F L S * 604

6061 TTTAGAATTAATTTATTAAATGTATTATAACTTTAACTTTTATCCTAATTTGGTTTCCTT 6120
6121 AAAATTTTTATTATTACAACTCAAAAAACATTGTTTTGTGTAACATATTATATATGT 6180
6181 ATCTAAACCATATGAACATATATTTTTTAGAACTAAGAGAATGATAGGCTTTTGTTCCTT 6240
6241 ATGAACGAAAAAGAGGTAGCACTACAAACACAATATTCAATCAAAATTTTCAGCATTATTG 6300
6301 AAATTGTAAGTGAAGTAAACTTAAGATATTTGAGTTAACCTTTAAGAATTTTAAATATT 6360
6361 TTGGCATTGTACTAATACCGGGAACATGAAGCCAGGTGTGGTGGTATGTGCCTGTAGTCC 6420
6421 CAGGCTGAGGCAAGAGAATTACTTGAGCCCAGGAGTTTGAATCCATCCTGGGCAGCATAC 6480
6481 TGAGACCCTGCCTTTAAAAACAAACAGAACAAAAACAAACACCAGGGACACATTTCTCT 6540
6541 GTCTTTTTTGATCAGTGCCTATACATCGAAGGTGTGCATATATGTTGAATCACATTTTA 6600
6601 GGGACATGGTGTTTTTATAAAGAATTCTGTGAGAAAAAATTTAATAAAGCAACCAAAAAA 6660
6661 AAAAAAAA 6669

Fig. 2 (cont.)

T0600T" 25542600

SEQ. ID 7-1 GAGCGCCCGGG¹~~CT~~²GATCCGAGCCGAGCGGGCCGTATCTCCTTGTCGGCGCCGCTGATTCC 60
 61 CGGCTCTGCGGAGGCCTCTAGGCAGCCGCGCAGCTTCCGTGTTTGCTGCGCCCGCACTGC 120
 121 ~~G~~²~~A~~³TTTACAACCCTGAAGAATCTCCCTATCCCTATTTTGTCCCCCTGCAGTAATAAATCCC 180
 181 ATTATGGAGATCTCGAACTTTATAAAGGGATATAGTTTGAATTCTATGGAGTGTAATTT 240
 241 TGTGTATGAATTATATTTTTTAAACATTGAAGAGTTTTTCAGAAAGAAGGCTAGTAGAGTT 300
 301 GATTACTGATACTTTATGCTAAGCAGTACTTTTTTGGTAGTACAATATTTTGTAGGCGT 360
 361 TTCTGATAACACTAGAAAGGACAAGTTTTATCTTGTGATAAATTGATTAATGTTTACAAC 420
 421 ATGACTGATAATTATAGCTGAATAGTCCTTAAATGATGAACAGGTTATTTAGTTTTTAAA 480
 481 TGCAGTGTAAGAGTGTGCTGTGGAAATTTTATGGCTAACTAAGTTTATGGAGAAAATAC 540
 541 CTTCAAGTTGATCAAGAATAATAGTGGTATACAAAGTTAGGAAGAAAGTCAACATGATGCT 600
 601 GCAGGAAATGGAAACAAATACAAATGATATTTAACAAGATAGAGTTTACAGTTTTTGAA 660
 661 CTTTAAGCCAAATTCATTTGACATCAAGCACTATAGCAGGCACAGGTTCAACAAAGCTTG 720
 721 TGGGTATTGACTTCCCCCAAAGTTGTGAGCTGAAGTAATTTAGCCCACTTAAGTAAATA 780
 781 CTATGATGATAAGCTGTGTGAAGTTAGCTTTTAAATAGTGTGACCATATGAAGGTTTTAA 840
 841 TTACTTTTGTATTATTGGAATAAAATGAGATTTTTTGGGTTGTGATGTTAAAGTGCTTATA 900
 901 GGGAAAGAAGCCTGCATATAATTTTTTACCTTGTGGCATAATCAGTAATTGGTCTGTTAT 960
 961 TCAGGCTTCATAGCTTGTAAACARATATAAATAAAAGGCATAATTTAGGTATTCTATAGT 1020
 1021 TGCTTAGAATTTTGTAAATATAAATCTCTGTGAAAAATCAAGGAGTTTTAATATTTTCAG 1080
 1081 AAGTGCATCCACCTTTTCAGGGCTTAAAGTTAGTATTAACCAAGATTATGAACAAATAGC 1140
 1141 ACTTAGGTTACCTGAAAGAGTTACTACAACCCCAAAGAGTTGTGTTCTAAGTAGTATCTT 1200
 1201 GGTAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAATCCAGTAAAGAA 1260
 1261 AGTGTAGTAAATTCTACATAAGAGTCTATCATTGATTTCTTTTTGTGGTAAAAATCTTAG 1320
 1321 TTCATGTGAAGAAATTTTCATGTGAATGTTTTAGCTATCAAACAGTACTGTCACCTACTCA 1380
 1381 TGCACAAAACCTGCCTCCCAAAGACTTTTCCCAGGTCCCTCGTATCAAACATTAAAGAGTA^M 1440
 SEQ. ID 8-2 H K T A S Q R L F P G P S Y Q N I K S I 21
 1441 TAATGGAAGATAGCAGGATCTTGTGAGATTGGACAAACAGCAACAAACAAAAATGAAGT 1500
 22 M E D S T I L S D W T N S N K Q K M K Y 41
 1501 ATGACTTTTCTGTGAAGTCTACAGAAATGTCTACATATTCAACTTTCCCGCCGGGGTGC 1560
 42 D F S C E L Y R M S T Y S T F P A G V P 61
 1561 CTGTCTCAGAAAGGAGTCTTGCTCGTGCTGGTTTTTATTATACTGGTGTGAATGACAAGG 1620
 62 V S E R S L A R A G F Y Y T G V N D K V 81
 1621 TCAAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAACTAGGAGACAGTCCTATTTC 1680
 82 K C F C C G L M L D N W K L G D S P I Q 101
 1681 AAAAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTCAGAATCTGGTTTTCAGCTAGTC 1740
 102 K H K Q L Y P S C S F I Q N L V S A S L 121
 1741 TGGGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTGCACATTCATTATCTC 1800
 122 G S T S K N T S P M R N S F A H S L S P 141
 1801 CCACCTTGGAACATAGTAGCTTGTTCAGTGGTTCTTACTCCAGCCTTTCTCCAAACCCCTC 1860
 142 T L E H S S L F S G S Y S S L S P N P L 161
 1861 TTAATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAA 1920
 162 N S R A V E D I S S S R T N P Y S Y A M 181
 1921 TGAGTACTGAAGAAGCCAGATTTCTTACCTACCATATGTGGCCATTAACTTTTTTGTAC 1980
 182 S T E E A R F L T Y H M W P L T F L S P 201

Fig. 3

9/33

1981 CATCAGAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGGTAGCCTGCT 2040
 202 S E L A R A G F Y Y I G P G D R V A C F 221

2041 TTGCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAGGATGATGCTATGTCAGAACACC 2100
 222 A C G G K L S N W E P K D D A M S E H R 241

2101 GGAGGCATTTTCCCAACTGTCCATTTTGGAAAATTCTCTAGAACTCTGAGGTTTAGCA 2160
 242 R H F P N C P F L E N S L E T L R F S I 261

2161 TTTCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTTATGTACTGGCCAT 2220
 262 S N L S M Q T H A A R M R T F M Y W P S 281

2221 CTAGTGTTCCAGTTCAGCCTGAGCAGCTTGCAAGTGTGGTTTTTATTATGTGGTTCGCA 2280
 282 S V P V Q P E Q L A S A G F Y Y V G R N 301

2281 ATGATGATGTCAAATGCTTTTGTGTGATGGTGGCTTGAGGTGTTGGGAATCTGGAGATG 2340
 302 D D V K C F C C D G G L R C W E S G D D 321

2341 ATCCATGGGTAGAACATGCCAAGTGGTTTCCAAGTGTGAGTTCTTGATACGAATGAAAG 2400
 322 P W V E H A K W F P R C E F L I R M K G 341

2401 GCCAAGAGTTTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGTGTGT 2460
 342 Q E F V D E I Q G R Y P H L L E Q L L S 361

2461 CAACTTCAGATACCACTGGAGAAGAAAATGCTGACCCACCAATTATTCATTTTGGACCTG 2520
 362 T S D T T G E E N A D P P I I H F G P G 381

2521 GAGAAAGTTCTTCAGAAGATGCTGTCATGATGAATACACCTGTGGTTAAATCTGCCTTGG 2580
 382 E S S S E D A V M M N T P V V K S A L E 401

2581 AAATGGGCTTTAATAGAGACCTGGTGAAACAAACAGTTCAAAGTAAAATCCTGACAACTG 2640
 402 M G F N R D L V K Q T V Q S K I L T T G 421

2641 GAGAGAACTATAAAACAGTTAATGATATTGTGTGACCACTTCTTAATGCTGAAGATGAAA 2700
 422 E N Y K T V N D I V S A L L N A E D E K 441

2701 AAAGAGAAGAGGAGAAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTGTGATTAA 2760
 442 R E E E K E K Q A E E M A S D D L S L I 461

2761 TTCGAAGAACAGAATGGCTCTCTTCAACAATTGACATGTGTGCTTCCTATCCTGGATA 2820
 462 R K N R M A L F Q Q L T C V L P I L D N 481

2821 ATCTTTTAAAGGCCAATGTAATTAATAAACAGGAACATGATATTATTAAACAAAAACAC 2880
 482 L L K A N V I N K Q E H D I I K Q K T Q 501

2881 AGATACCTTTACAAGCGAGAGAACTGATTGATACCATTTTGGTTAAAGGAAATGCTGCGG 2940
 502 I P L Q A R E L I D T I L V K G N A A A 521

2941 CCAACATCTTCAAAAAGTGTCTAAAAGAAATGACTCTACATTGTATAAGAACTTATTTG 3000
 522 N I F K N C L K E I D S T L Y K N L F V 541

3001 TGGATAAGAATATGAAGTATATCCCAACAGAAGATGTTTCAGTCTGTCACTGGAAGAAC 3060
 542 D K N M K Y I P T E D V S G L S L E E Q 561

Fig. 3 (cont.)

10/33

3061 AATTGAGGAGGTTGCAAGAAGAACGAACTTGTAAGTGTGTATGGACAAAGAAGTTTCTG 3120
562 L R R L Q E E R T C K V C M D K E V S V 581

3121 TTGTATTTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCTTCTCTAAGAA 3180
582 V F I P C G H L V V C Q E C A P S L R K 601

3181 AATGCCCTATTTGCAGGGGTATAATCAAGGGTACTGTTTCGTACATTTCTCTCTTAAAGAA 3240
602 C P I C R G I I K G T V R T F L S * 618

3241 AAATAGTCTATATTTTAACCTGCATAAAAAGGTCTTTAAATATTGTTGAACACTTGAAG 3300
3301 CCATCTAAAGTAAAAAGGAATTATGAGTTTTTCAATTAGTAACATTCATGTTCTAGTCT 3360
3361 GCTTTGGTACTAATAATCTTGTCTGAAAAGATGGTATCATATATTTAATCTTAATCTG 3420
3421 TTTATTTACAAGGGAAGATTTATGTTTGGTGAACATATTAGTATGTATGTGTACCTAAG 3480
3481 GGAGTAGTGTCACTGCTTGTATGCATCATTTTCAGGAGTTACTGGATTTGTTGTTCTTTC 3540
3541 AGAAAGCTTTGAATACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACCTGGAG 3600
3601 TTCATCAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTGTTTTAAATAAG 3660
3661 GATTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAA 3720
3721 AGAAAAAAAAAA 3732

Fig. 3 (cont.)

10/33

SEQ. ID 9-1 ATTTTAAATTGATGCATTAACATTCTAAACATTCTGTTTTTAAATAGTAAAAATT 60
 61 GAACTTGCCTTGAATATGTAATGATTCAATATAACAATTATGCATAGTCTTAAATAATC 120
 121 TGCATATTTTATGCTGCTTTTCATGTTTTTCTAATTAATGACTTCACATGTTAATATTT 180
 181 ATAATTTTCTGTCATAGTTTCCATATTTATATAAAATGAATACTTAAGATCAGTAATTC 240
 241 TGCTCTGTTTGTATATACTATTTTCCATCAAAAGACAAAATGGGACTGAGGTTGAGGC 300
 301 TCGTTGCTAAAGCACTTTCCTAAATGCAAAAGGCCCTATGATGGATCCCTAGTACTTAT 360
 361 TTAAGTGAGAGAGAAACAGGCTGGGGGTGTAGGTCTGTTAGAGCATGTGTTTGGCATTAT 420
 421 GTGAAGCCCAACACTAAAAAAGGAGAACAACAAGCGCAGACTTTAAACTCAAGTG 480
 481 GTTTGGTAATGTACGACTCTACTGTTTAGAATTAATAATGTGTCTTAGTTATTGTGCCATT 540
 541 ATTTTATGTCATCACTGGATAATATATTAGTGCTTAGTATCAGAAATAGTCCTTATGCT 600
 601 TTGTGTTTTGAAGTTCCTAATGCAATGTTCTCTTTCTAGAAAAGGTGGACAAGTCTATT 660
 661 TTCCAGAGAAGATGACTTTTAACAGTTTGAAGGAAGTGAAGTCTTTGTACTTGCAGACA 720
 SEQ. ID 10-1 M T F N S F E G T R T F V L A D T 17
 721 CCAATAAGGATGAAGAATTTGTAGAAGAGTTTAATAGATTAAAAACATTTGCTAATTC 780
 18 N K D E E F V E E F N R L K T F A N F P 37
 781 CAAGTAGTAGTCCTGTTTCAGCATCAACATTGGCGGAGCTGGGTTTCTTTATACCGGTG 840
 38 S S S P V S A S T L A R A G F L Y T G E 57
 841 AAGGAGACACCGTGCAATGTTTCAGTTGTCATGCGGCAATAGATAGATGGCAGTATGGAG 900
 58 G D T V Q C F S C H A A I D R W Q Y G D 77
 901 ACTCAGCTGTTGGAAGACACAGGAGAATATCCCCAAATTGCAGATTTATCAATGGTTTTT 960
 78 S A V G R H R R I S P N C R F I N G F Y 97
 961 ATTTTGAAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAAT 1020
 98 F E N G A A Q S T N P G I Q N G Q Y K S 117
 1021 CTGAAAATGTTGTTGGGAAATAGAAATCCTTTTGCCCTGACAGGCCACCTGAGACTCATG 1080
 118 E N C V G N R N P F A P D R P P E T H A 137
 1081 CTGATTATCTCTTGAGAACTGGACAGGTTGTAGATATTTAGACACCATATACCCGAGGA 1140
 138 D Y L L R T G Q V V D I S D T I Y P R N 157
 1141 ACCCTGCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTTAGAACTGGCCGGACTATG 1200
 158 P A M C S E E A R L K S F Q N W P D Y A 177
 1201 CTCATTTAACCCCAAGAGAGTTAGCTAGTGCTGGCCTCTACTACACAGGGGCTGATGATC 1260
 178 H L T P R E L A S A G L Y Y T G A D D Q 197
 1261 AAGTGCAATGCTTTTGTGTGGGGGAAAATGAAAATTTGGGAACCTGTGATCGTGCTT 1320
 198 V Q C F C C G G K L K N W E P C D R A W 217
 1321 GGTGAGAACACAGGAGACACTTTCCCAATTGCTTTTTTGTGTTTGGGCCGGAACGTTAATG 1380
 218 S E H R R H F P N C F F V L G R N V N V 237
 1381 TTCGAAGTGAATCTGGTGTGAGTTCTGATAGGAATTTCCCAAATTCACAACTCTCCAA 1440
 238 R S E S G V S S D R N F P N S T N S P R 257
 1441 GAAATCCAGCCATGGCAGAATATGAAGCACGGATCGTTACTTTTGAACATGGACATCCT 1500
 258 N P A M A E Y E A R I V T F G T W T S S 277

Fig. 4

FIGURE 4

12/33

1501 CAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAG 1560
278 V N K E Q L A R A G F Y A L G E G D K V 297

1561 TGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGG 1620
298 K C F H C G G G L T D W K P S E D P W D 317

1621 ACCAGCATGCTAAGTGCTACCCAGGGTGTCAAATACCTATTGGATGAGAAGGGGCAAGAAT 1680
318 Q H A K C Y P G C K Y L L D E K G Q E Y 337

1681 ATATAAATAATATTCATTTAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAA 1740
338 I N N I H L T H P L E E S L G R T A E K 357

1741 AAACACCACCGCTAACTAAAAAATCGATGATACCATCTTCCAGAATCCTATGGTGCAAG 1800
358 T P P L T K K I D D T I F Q N P M V Q E 377

1801 AAGCTATACGAATGGGATTTAGCTTCAAGGACCTTAAGAAAACAATGGAAGAAAAAATCC 1860
378 A I R M G F S F K D L K K T M E E K I Q 397

1861 AAACATCCGGGAGCAGCTATCTATCACTTGAGGTCCTGATTGCAGATCTTGTGAGTGCTC 1920
398 T S G S S Y L S L E V L I A D L V S A Q 417

1921 AGAAAGATAATACGGAGGATGAGTCAAGTCAAACCTTCATTGCAGAAAGACATTAGTACTG 1980
418 K D N T E D E S S Q T S L Q K D I S T E 437

1981 AAGAGCAGCTAAGGCGCCTACAAGAGGAGAAGCTTTCCAAAATCTGTATGGATAGAAATA 2040
438 E Q L R R L Q E E K L S K I C M D R N I 457

2041 TTGCTATCGTTTTTTTTTCTTGTGGACATCTGGCCACTTGTAACAGTGTGCAGAAGCAG 2100
458 A I V F F P C G H L A T C K Q C A E A V 477

2101 TTGACAAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAAAATTTTTATGTCTT 2160
478 D K C P M C Y T V I T F N Q K I F M S * 496

2161 AGTGGGGCACCACATGTTATGTTCTTCTTGCTCTAATTGAATGTGTAATGGGAGCGAACT 2220
2221 TTAAGTAATCCTGCATTTGCATTCCATTAGCATCCTGCTGTTTCCAAATGGAGACCAATG 2280
2281 CTAACAGCACTGTTTCCGTCTAAACATTCAATTTCTGGATCTTTTCGAGTTATCAGCTGTA 2340
2341 TCATTTAGCCAGTGTCTTACTCGATTGAAACCTTAGACAGAGAAGCATTTTATAGCTTTT 2400
2401 CACATGTATATTGGTAGTACACTGACTTGATTTCTATATGTAAGTGAATTCATCACCTGC 2460
2461 ATGTTTCATGCCTTTTGCATAAGCTTAACAAATGGAGTGTCTGTATAAGCATGGAGATG 2520
2521 TGATGGAATCTGCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAAGAACTGCCCCA 2580
2581 CGCTGCTGGGAGGATAAAGATTGTTTTAGATGCTCACTTCTGTGTTTTAGGATTCTGCCC 2640
2641 ATTTACTTGAATTTATTGGAGTTATAATGTACTTATATGATATTCCGAA 2691

Fig. 4 (cont.)

Fig. 5

14/33

1261 TGCTCAGAATCAAAGGCCAAGAATTTGTCTAGCCAAAGTTCAAGCTGGCTATCCTCATCTAC 1320
 321 L R I K G Q E F V S Q V Q A G Y P H L L 340
 1321 TTGAGCAGCTATTATCTACGTCAGACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCG 1380
 341 E Q L L S T S D S P E D E N A D A A I V 360
 1381 TGCATTTTGGCCCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCACGCCTGTGGTTA 1440
 361 H F G P G E S S E D V V M M S T P V V K 380
 1441 AAGCAGCCTTGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGCGGCAGA 1500
 381 A A L E M G F S R S L V R Q T V Q R Q I 400
 1501 TCCTGGCCACTGGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATG 1560
 401 L A T G E N Y R T V S D L V I G L L D A 420
 1561 CAGAAGACGAGATGAGAGAGGAGCAGATGGAGCAGGCGGCCGAGGAGGAGGAGTCAGATG 1620
 421 E D E M R E E Q M E Q A A E E E E S D D 440
 1621 ATCTAGCACTAATCCGGAAGAACAAAATGGTGCTTTTCCAACATTTGACGTGTGTGACAC 1680
 441 L A L I R K N K M V L F Q H L T C V T P 460
 1681 CAATGCTGTATTGCCTCCTAAGTGCAAGGGCCATCACTGAACAGGAGTGCAATGCTGTGA 1740
 461 M L Y C L L S A R A I T E Q E C N A V K 480
 1741 AACAGAAACCACACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAA 1800
 481 Q K P H T L Q A S T L I D T V L A K G N 500
 1801 ACACTGCAGCAACCTCATTGAGAACTCCCTTCGGGAAATTGACCCTGCGTTATACAGAG 1860
 501 T A A T S F R N S L R E I D P A L Y R D 520
 1861 ATATATTTGTGCAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAA 1920
 521 I F V Q Q D I R S L P T D D I A A L P M 540
 1921 TGGAAGAACAGTTGCGGAACTCCAGGAGGAAAGAATGTGTAAAGTGTGTATGGACCGAG 1980
 541 E E Q L R K L Q E E R M C K V C M D R E 560
 1981 AGGTATCCATCGTGTTCATTCCCTGTGGCCATCTGGTCGTGTGCAAAGACTGCGCTCCCT 2040
 561 V S I V F I P C G H L V V C K D C A P S 580
 2041 CTCTGAGGAAGTGTCCTATCTGTAGAGGGACCATCAAGGGCAGAGTGGGCACATTTCTCT 2100
 581 L R K C P I C R G T I K G T V R T F L S 600
 2101 CCTGAACAAGACTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCAGTGTCACT 2160
 *
 2161 CCCAGCTCCATTTCGGAAGTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACACACA 2220
 2221 AATATAAACATGAAAACTTTTGTCTGAAGTCAAGAATGAATGAATTACTTATATAATAA 2280
 2281 TTTTAATTGGTTTCTTAAAGTGCTATTTGTTCCCAACTCAGAAAATTGTTTCTGTAA 2340
 2341 ACATATTTACATACTACCTGCATCTAAAGTATTCATATATTCATATATTCAGATGTCATG 2400
 2401 AGAGAGGGTTTTGTTCTTGTTCCTGAAAAGCAGGGATTGCCTGCACTCCTGAAATTTCTCA 2460
 2461 GAAAGATTTACAATGTTGGCATTATGGTTTCAGAACTAGAATCTTCTCCGTTGCTTTA 2520
 2521 AGAACCGGGAGCACAGATGTCCATGTGTTTTATGTATAGAAATTCCTGTTATTTATTGGA 2580
 2581 TGACATTTTAGGGATATGAAATTTTTATAAAGAATTTGTGAGAAAAAGTTAATAAGCAA 2640
 2641 CATAATTACCTCTTTTTTTTTTAAAGAAAAA 2676

Fig. 5 (cont.)

SEQ. ID 13-1 AGTTATATAAAATACGAAGTTTTCAAAAAGAAGGCTAGTGCAACAGAAAAGCTTTGCTAA 60
 61 AACAGATTCTTAGTTATTTGAGGTAACAAAAGAAAGCCATGTCTTGAATTGATTGCTTCT 120
 121 TAATTATAACAGACTTATAGTGGAAGGGCCTTAAACACAGGCGGACTTTATAAAATGCA 180
 181 GTCTTAGGTTTATGTGCAAAATACTGTCTGTTGACCAGATGTATTCACATGATATATACA 240
 241 GAGTCAAGGTGGTGATATAGAAGATTTAACAGTGAGGGAGTTAACAGTCTGTGCTTTAAG 300
 301 CGCAGTTCCTTTACAGTGAATACTGTAGTCTTAATAGACCTGAGCTGACTGCTGCAGTTG 360
 361 ATGTAACCCACTTTAGAGAATACTGTATGACATCTTCTCTAAGGAAAACCAGCTGCAGAC 420
 421 TTCACTCAGTTCCTTTCAATTCATAGGAAAAGGAGTAGTTTCAGATGTCATGTTTAAGTCC 480
 481 TTATAAGGGAAAAGAGCCTGAATATATGCCCTAGTACCTAGGCTTCATAACTAGTAATAA 540
 541 GAAGTTAGTTATGGGTAAATAGATCTCAGGTTACCCAGAAGAGTTTCATGTGACCCCCAAA 600
 601 GAGTCCTAACTAGTGTCTTTGGCAAGTGAGACAGATTTGTCTGTGAGGGTGTCAATTCAC 660
 661 CAGTCCAAGCAGAAGACAATGAATCTATCCAGTCAGGTGTCTGTGGTGGAGATCTAGTGT 720
 721 CCAAGTGGTGAGAACTTCATCTGGAAGTTTAAGCGGTGAGAAATACTATTACTACTCAT 780
 1 M 1

781 GGACAAAACGTCTCTCCAGAGACTCGGCCAAGGTACCTTACACCAAAAACCTTAAACGTAT 840
 SEQ. ID 14-2 D K T V S Q R L G Q G T L H Q K L K R I 21

841 AATGGAGAAGAGCACAATCTTGTCAAATTGGACAAAGGAGAGCGAAGAAAAATGAAGTT 900
 22 M E K S T I L S N W T K E S E E K M K F 41

901 TGACTTTTCGTGTGAACCTCTACCGAATGTCTACATATTCAGCTTTTCCAGGGGAGTTCC 960
 42 D F S C E L Y R M S T Y S A F P R G V P 61

961 TGTCTCAGAGAGGAGTCTGGCTCGTGCTGGCTTTTATTATACAGGTGTGAATGACAAAGT 1020
 62 V S E R S L A R A G F Y Y T G V N D K V 81

1021 CAAGTGCTTCTGCTGTGGCCTGATGTTGGATAACTGGAACAAGGGGACAGTCTCTGTTGA 1080
 82 K C F C C G L M L D N W K Q G D S P V E 101

1081 AAAGCACAGACAGTTCTATCCCAGCTGCAGCTTTGTACAGACTCTGCTTTTCAGCCAGTCT 1140
 102 K H R Q F Y P S C S F V Q T L L S A S L 121

1141 GCAGTCTCCATCTAAGAATATGTCTCCTGTGAAAAGTAGATTTGCACATTCGTCACCTCT 1200
 122 Q S P S K N M S P V K S R F A H S S P L 141

1201 GGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCCTCTTAATTCTAGAGCAGTGGA 1260
 142 E R G G I H S N L C S S P L N S R A V E 161

1261 AGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCATGAGTACAGAAGAGGCCAGATT 1320
 162 D F S S R M D P C S Y A M S T E E A R F 181

1321 TCTTACTTACAGTATGTGGCCTTTAAGTTTTCTGTCAACAGCAGAGCTGGCCAGAGCTGG 1380
 182 L T Y S M W P L S F L S P A E L A R A G 201

1381 CTTCTATTACATAGGGCCTGGAGACAGGGTGGCCTGTTTTGCCTGTGGTGGGAAACTGAG 1440
 202 F Y Y I G P G D R V A C F A C G G K L S 221

1441 CAACTGGGAACCAAAGGATGATGCTATGTCAGAGCACCGCAGACATTTTCCCCACTGTCC 1500
 222 N W E P K D D A M S E H R R H F P H C P 241

1501 ATTTCTGGAAAATACTTCAGAAACACAGAGGTTTAGTATATCAAATCTAAGTATGCAGAC 1560
 242 F L E N T S E T Q R F S I S N L S M Q T 261

Fig. 6

16/33

1561 ACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACCTAGTGTTCTGTTTCAGCCCCGA 1620
 262 H S A R L R T F L Y W P P S V P V Q P E 281

1621 GCAGCTTGCAAGTCTGGATTCTATTACGTGGATCGCAATGATGATGTCAAGTGCTTTTG 1680
 282 Q L A S A G F Y Y V D R N D D V K C F C 301

1681 TTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGACCCCTGGATAGAACACGCCAA 1740
 302 C D G G L R C W E P G D D P W I E H A K 321

1741 ATGGTTTCCAAG¹GTGTGAGTTCTTGATACGGATGAAGGGTCAGGAGTTTGTGATGAGAT 1800
 322 W F P R C E F L I R M K G Q E F V D E I 341

1801 TCAAGCTAGATATCCTCATCTTCTTGAGCAG²CTGTTGTCCACTTCAGACACCCCAGGAGA 1860
 342 Q A R Y P H L L E Q L L S T S D T P G E 361

1861 AGAAAATGCTGACCCCTACAGAGACAGTGGTGCATTTTGGCCCTGGAGAAAGTTTCGAAAGA 1920
 362 E N A D P T E T V V H F G P G E S S K D 381

1921 TGTCGTCATGATGAGCACGCCTGTGGTTAAAGCAGCCTTGGAATGGGCTTCAGTAGGAG 1980
 382 V V M M S T P V V K A A L E M G F S R S 401

1981 CCTGGTGAGACAGACGGTTCAGCGGCAGATCCTGGCCACTGGTGAGAACTACAGGACCGT 2040
 402 L V R Q T V Q R Q I L A T G E N Y R T V 421

2041 CAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGAGAGAAGAGAAGAGGAGAAGGA 2100
 422 N D I V S V L L N A E D E R R E E E K E 441

2101 AAGACAGACTGAAGAGATGGCATCAG⁴GTGACTTATCACTGATTCCGAAGAATAGAATGGC 2160
 442 R Q T E E M A S G D L S L I R K N R M A 461

2161 CCTCTTTCAACAGTTGACACATGTCCTTCCTATCCTGGATAATCTTCTTGAGGCCAGTGT 2220
 462 L F Q Q L T H V L P I L D N L L E A S V 481

2221 AATTACAAAACAGGAACATGATATTATTAGACAGAAAACACAGATACCCCTTACAAGCAAG 2280
 482 I T K Q E H D I I R Q K T Q I P L Q A R 501

2281 AGAGCTTATTGACACCGTTTTAGTCAAGGGAAATGCTGCAGCCAACATCTTCAAAAACCTC 2340
 502 E L I D T V L V K G N A A A N I F K N S 521

2341 TCTGAAGGAAATTGACTCCACGTTATATGAAAACCTTATTTG⁵TGGAAAAGAATATGAAGTA 2400
 522 L K E I D S T L Y E N L F V E K N M K Y 541

2401 TATTC AACAGAAGACGTTTCA⁶GGCTTGTCATTGGAAGAGCAGTTGCGGAGATTACAAGA 2460
 542 I P T E D V S G L S L E E Q L R R L Q E 561

2461 AGAACGAACTTGCAAAGTGTGTATGGACAGAGAGGTTTCTATTGTGTTTATTCCGTGTGG 2520
 562 E R T C K V C M D R E V S I V F I P C G 581

2521 TCATCTAGTAGTCTGCCAGGAATGTGCCCCCTTCTCTAAGGAAGTGCCCCATCTGCAGGGG 2580
 582 H L V V C Q E C A P S L R K C P I C R G 601

2581 GACAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGTGAAGAATGGTCTGAAAGTATT 2640
 602 T I K G T V R T F L S * 612

Fig. 6 (cont.)

2641 GTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACTACTGATTTTCAGCTCTTCAGCAGG 2700
2701 ACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTATGAAGGGTAGCATTGTATATTT 2760
2761 AAGCTTAGTCTGTTGCAAGGGAAGGTCTATGCTGTTGAGCTACAGGACTGTGTCTGTTCC 2820
2821 AGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGACTTCTTGGATTGGAATTTGT 2880
2881 GAAAGCTTTGGATTTCAGGTGATGTGGAGCTCAGAAATCCTGAAACCAGTGGCTCTGGTAC 2940
2941 TCAGTAGTTAGGGTACCCTGTGCTTCTTGCTGCTTTTCCTTTCTGGAAAATAAGGATTTT 3000
3001 TCTGCTACTGGTAAATATTTTCTGTTTGTGAGAAATATATTAAAGTGTTCCTTTTAAAGG 3060
3061 CGTGCATCATTGTAGTGTGTGCAGGGATGTATGCAGGCAAAACACTGTGTATATAATAAA 3120
3121 TAAATCTTTTTTAAAAAGTGTAACAAAAA 3151

Fig. 6 (cont.)

T000T 2542660

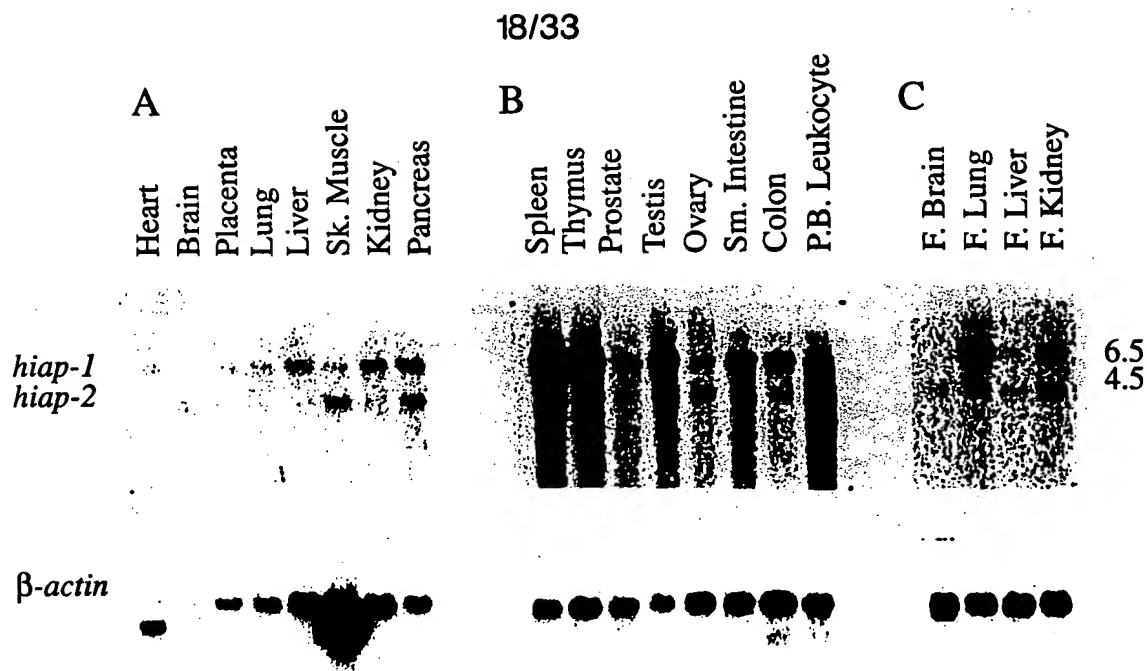


Fig. 7

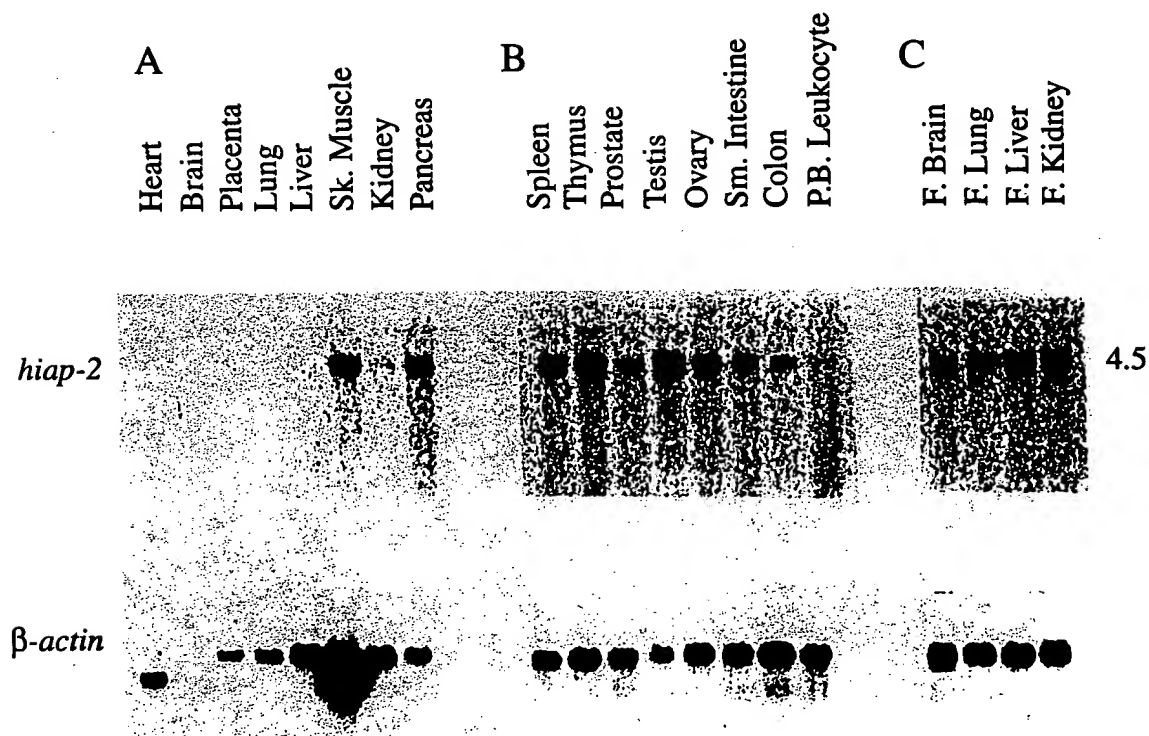


Fig. 8

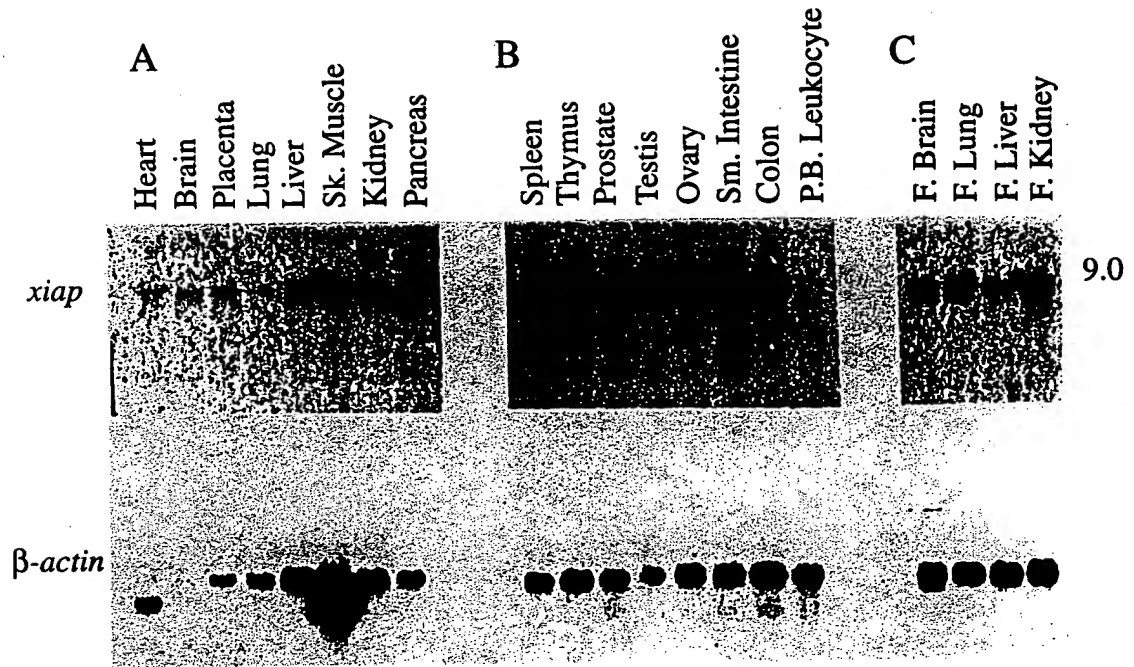


Fig. 9

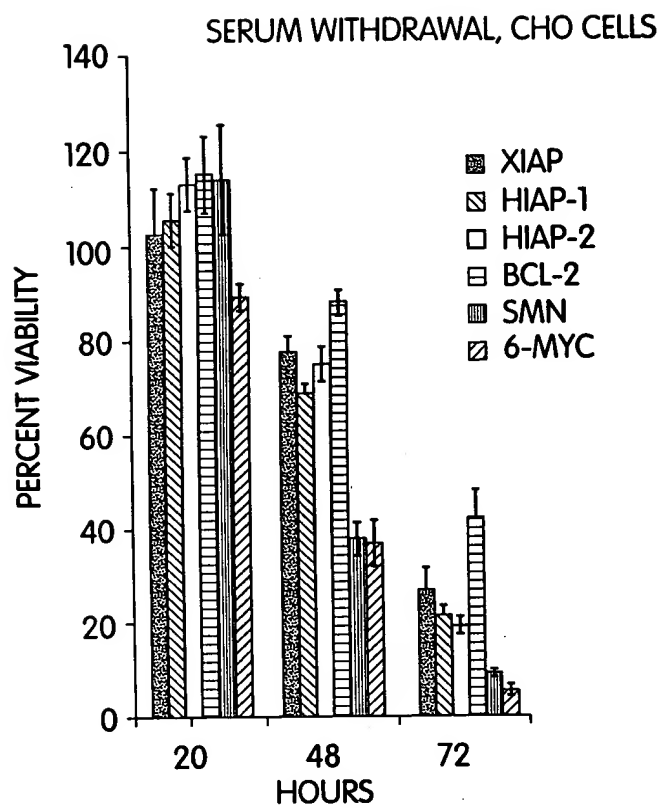


Fig. 10A

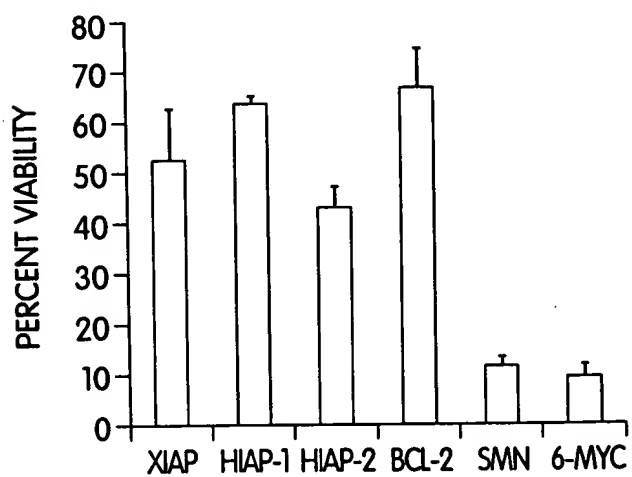
MENADIONE (20 μ M), CHO CELLS. 24hr SURVIVAL

Fig. 10B

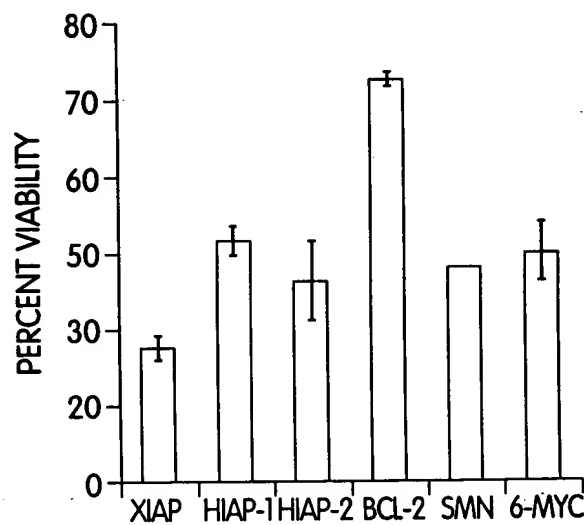
STAUROSPORINE ($1\mu\text{M}$), RAT-1 CELLS, 24 HOUR SURVIVAL

Fig. 10C

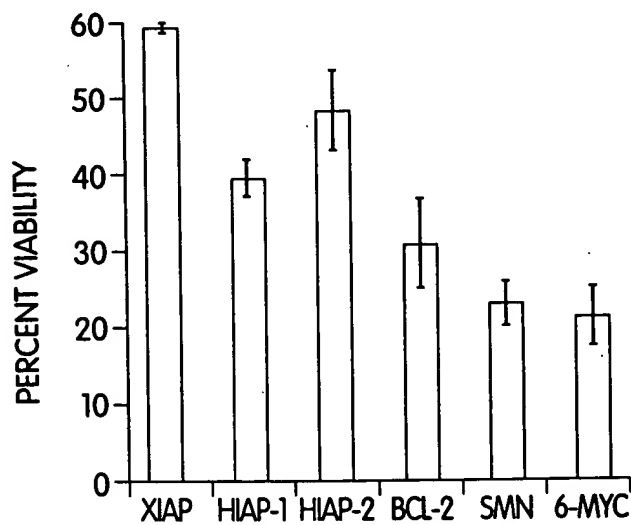
MENADIONE ($10\mu\text{M}$), RAT-1 CELLS, 18 HOUR SURVIVAL

Fig. 10D

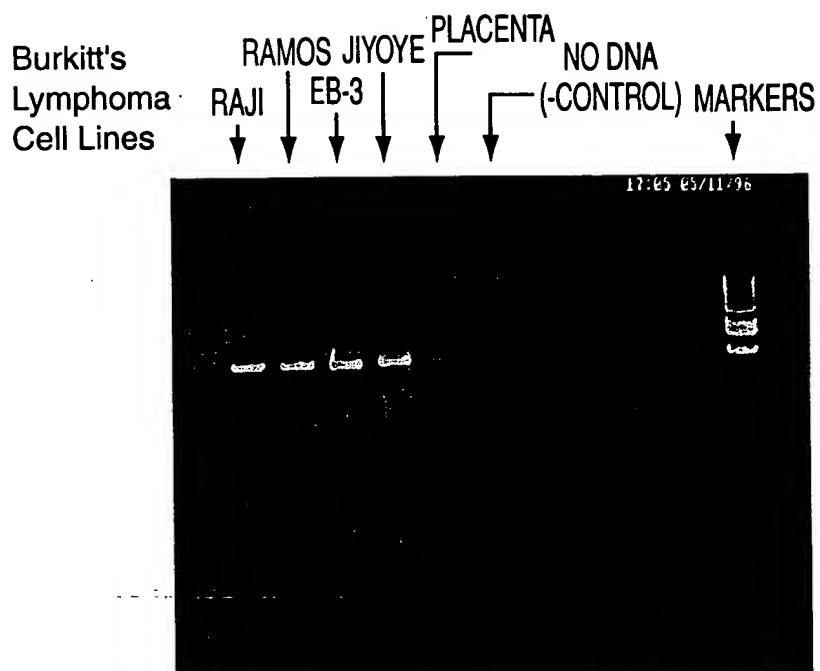


Fig. 11

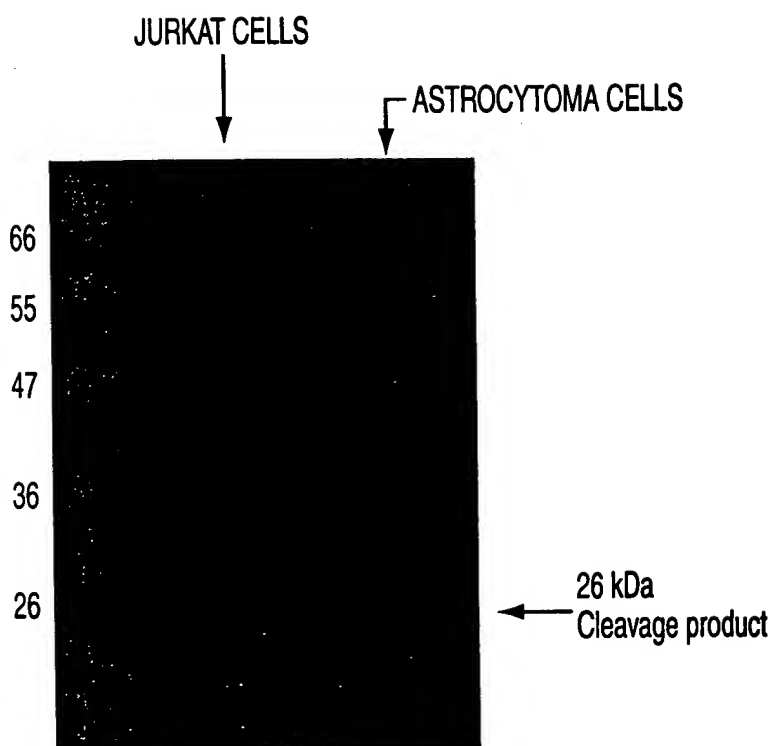


Fig. 12

23/33

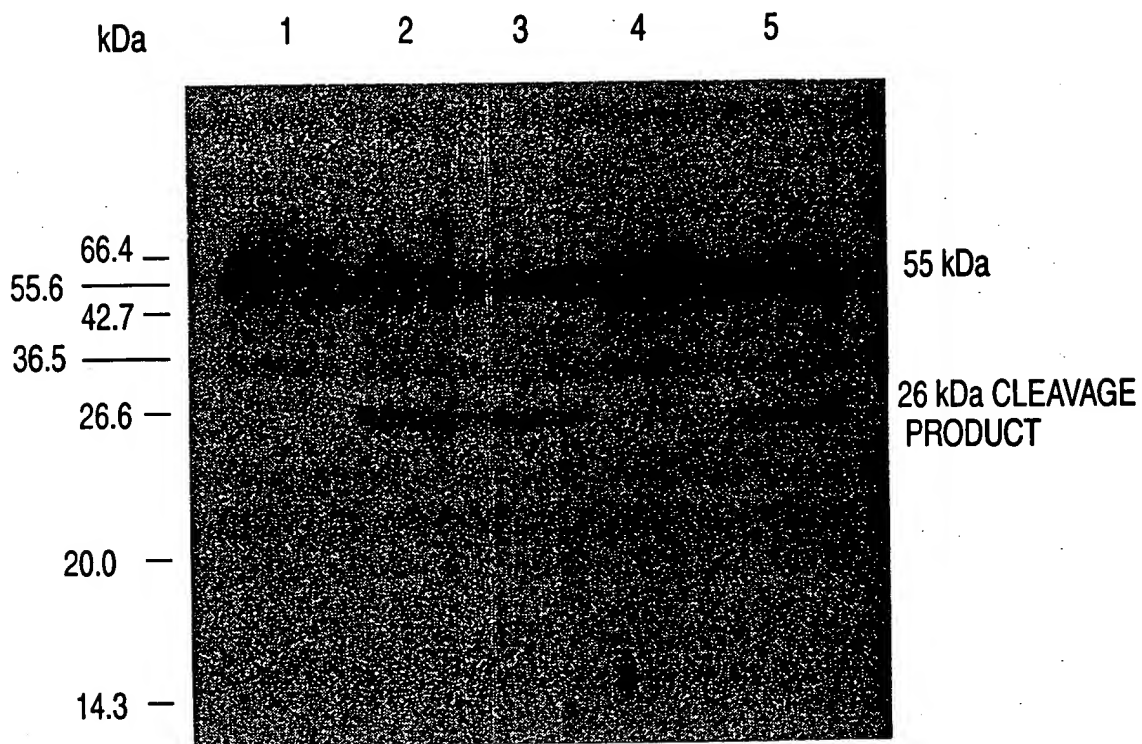


Fig. 13

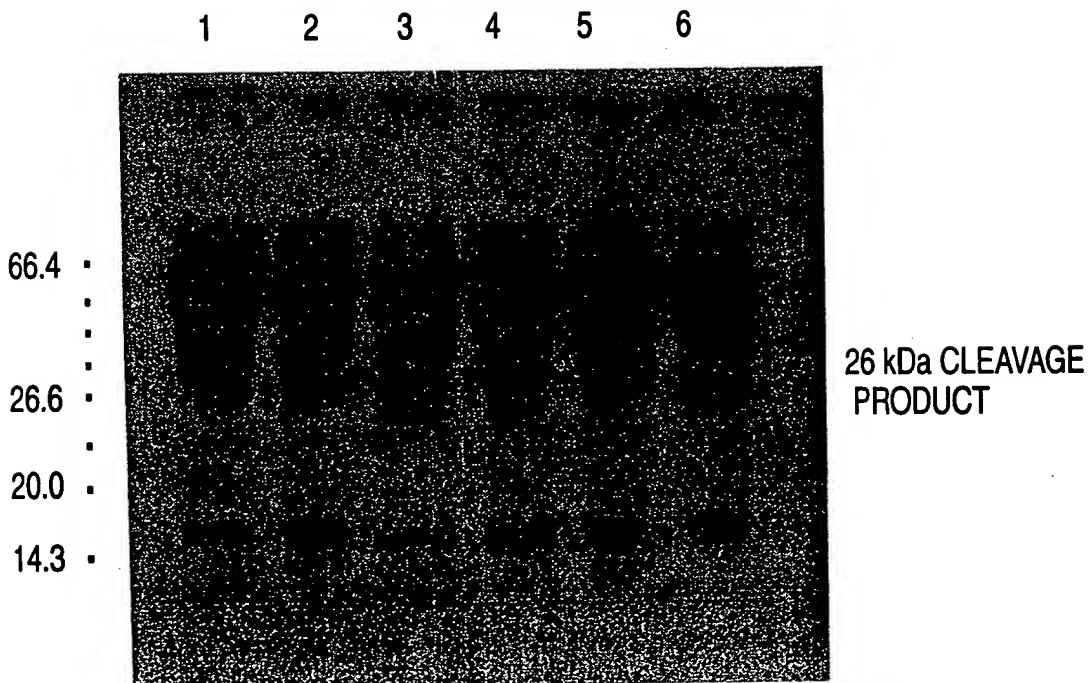
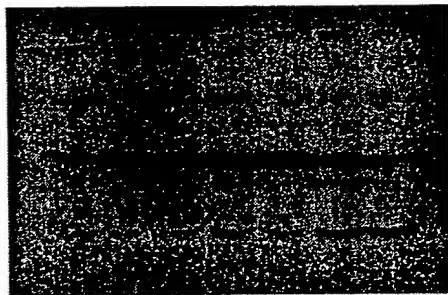


Fig. 14

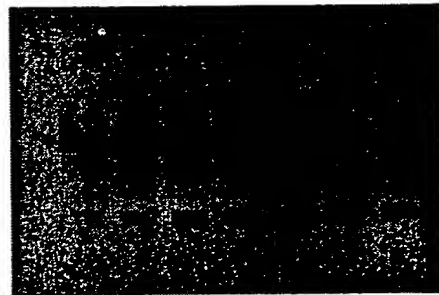
FOOT " 2057650

HeLa
M 0 1 2 3 5 10 22 (Hours)



-26 kDa

Jurkat
M 0 1 2 3 5 10 22 (Hours)



-26 kDa

Fig. 15A

Fig. 15B

2000T 254260

3 HOURS
HOURS 0 3 7 Cyto. Nucl.

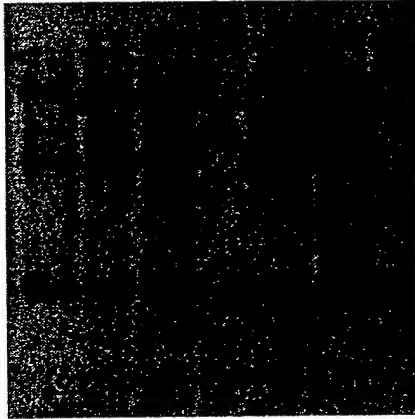
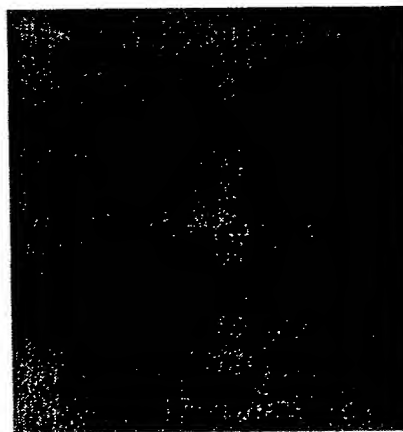


Fig. 16A

3 HOURS
MARKERS 0 3 7 Cyto. Nucl.

97.2 —
55.6 — 66.4 —
36.5 — 42.7 —
26.6 —



← 55 kDa

← 25 kDa

Fig. 16B

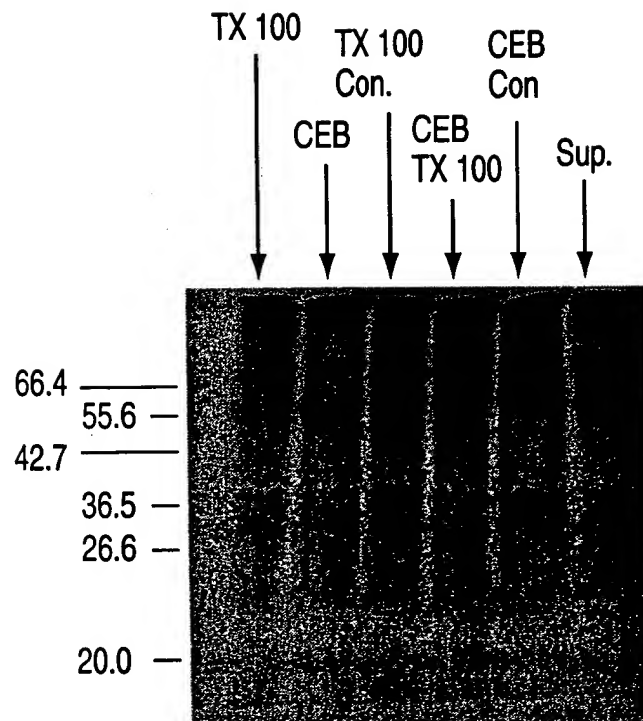


Fig. 17

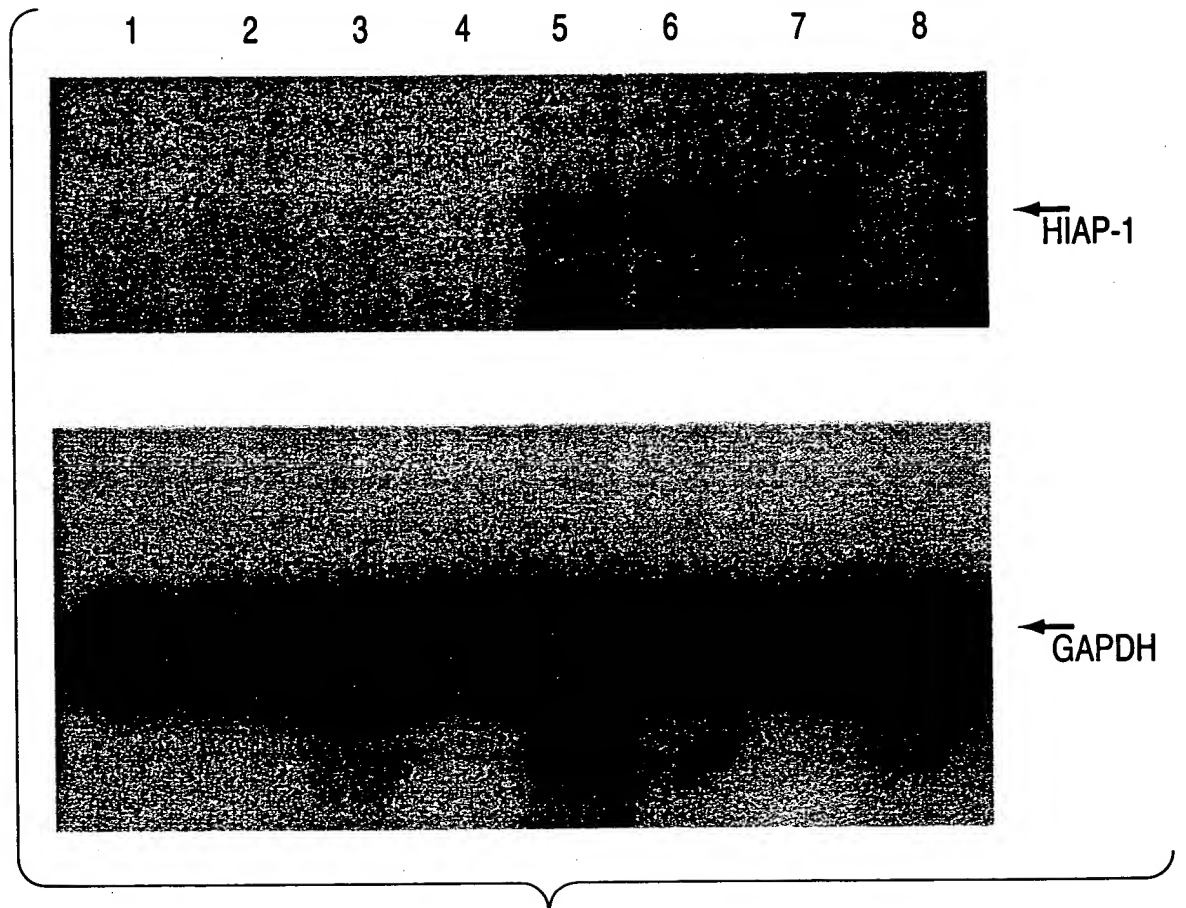


Fig. 18

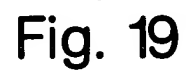




Fig. 20

2007-2-24-260

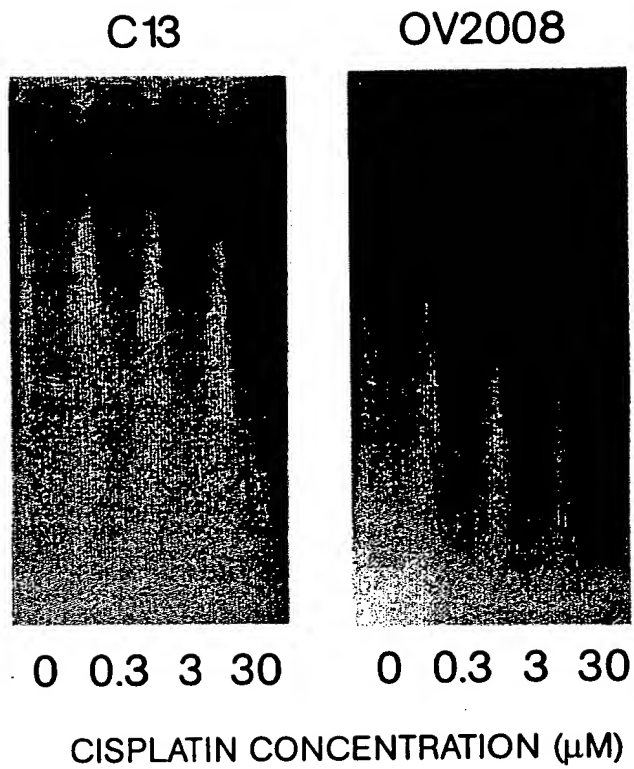


Fig. 21

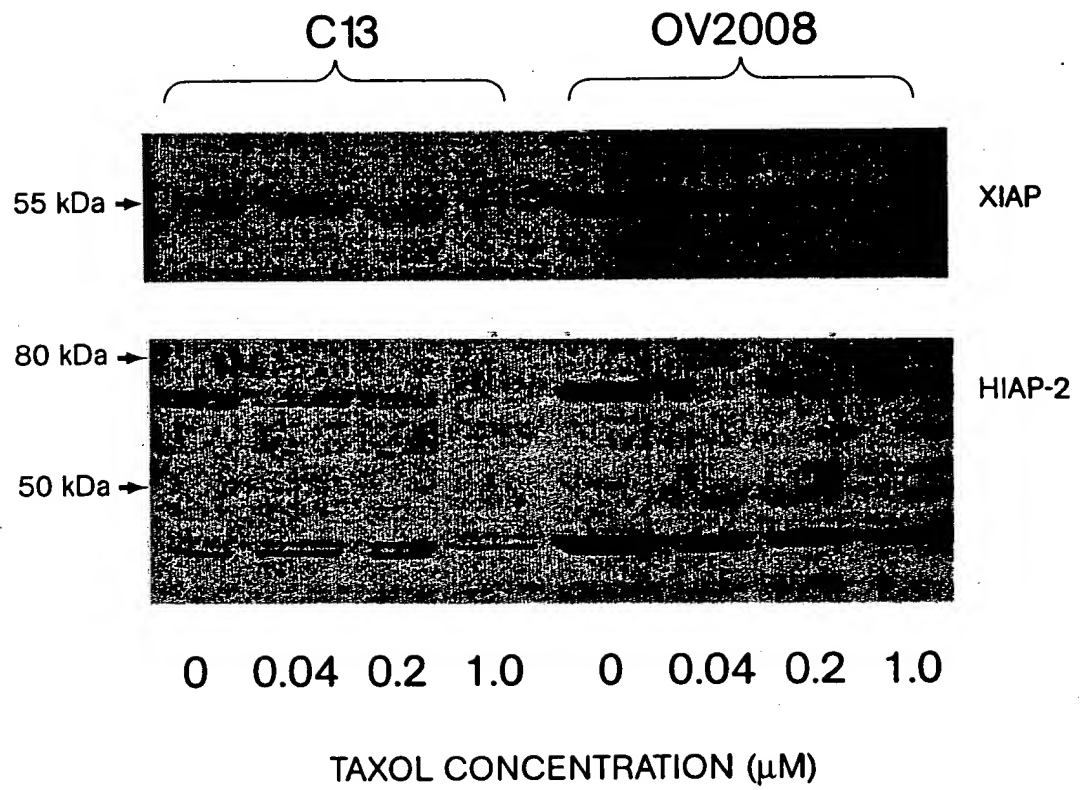


Fig. 22

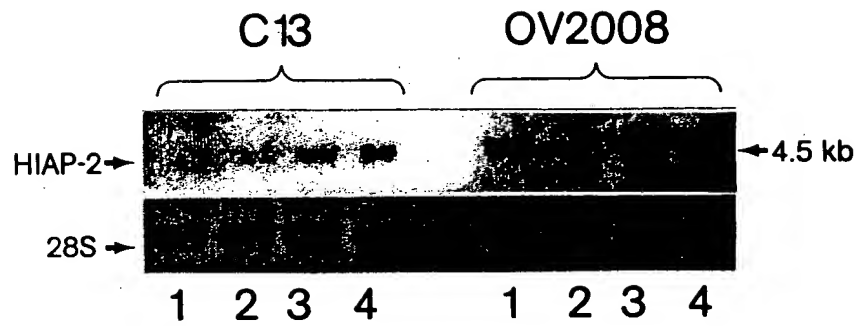


Fig. 23A

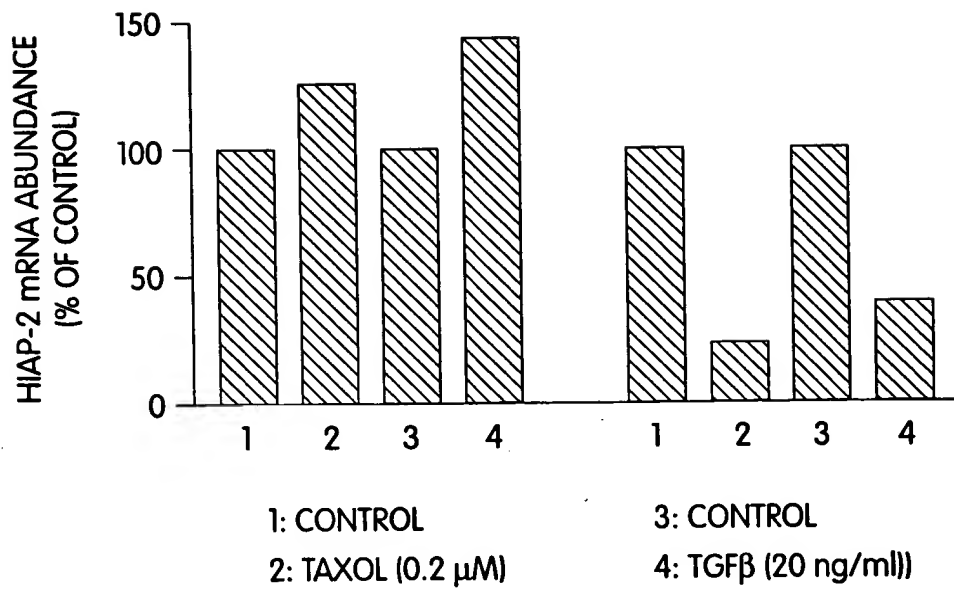


Fig. 23B

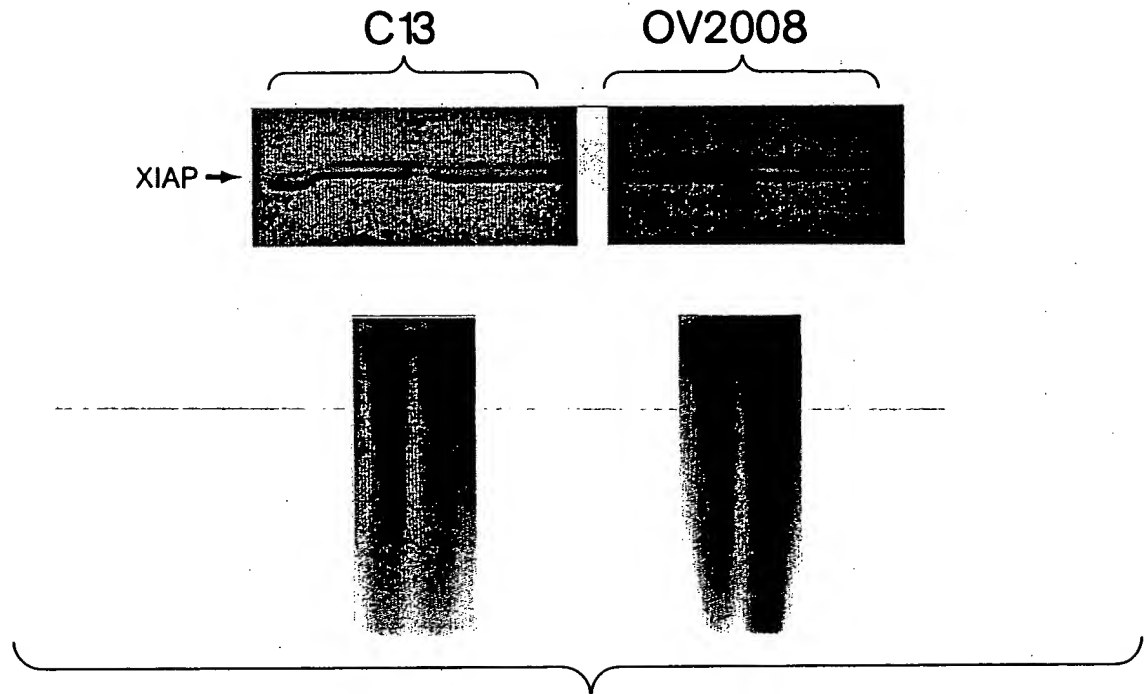


Fig. 24A

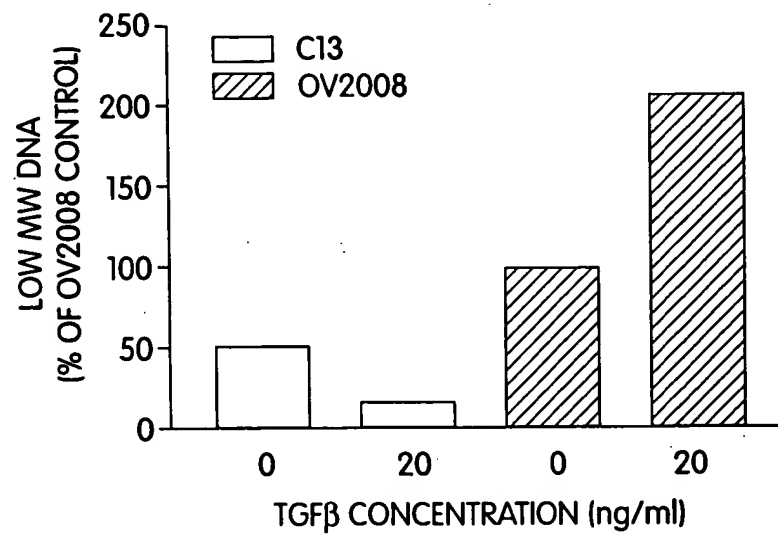


Fig. 24B